**Conclusions** Aspirin leads to dysbiosis of gut microbiota, which impairs the homeostasis of the intestinal mucosa (IDDF2022-ABS-0097 Figure 1X. Aspirin impairs intestinal homeostasis through gut microbiota metabolites axis). Supplement of probiotics *P. goldsteinii* may be a promising strategy to prevent Aspirin-induced GI damage.

IDDF2022-ABS-0155

## GLOBAL GENOME STUDY OF HELICOBACTER PYLORI PHAGE OPENS NEW PARADIGM ON THEIR WORLDWIDE DISTRIBUTION, GENETIC FEATURE, AND IMPACTS ON ANTIMICROBIAL RESISTANCE, DISEASE ADVANCEMENT, AND ACHIEVEMENT FOR PHAGE-BASED THERAPY

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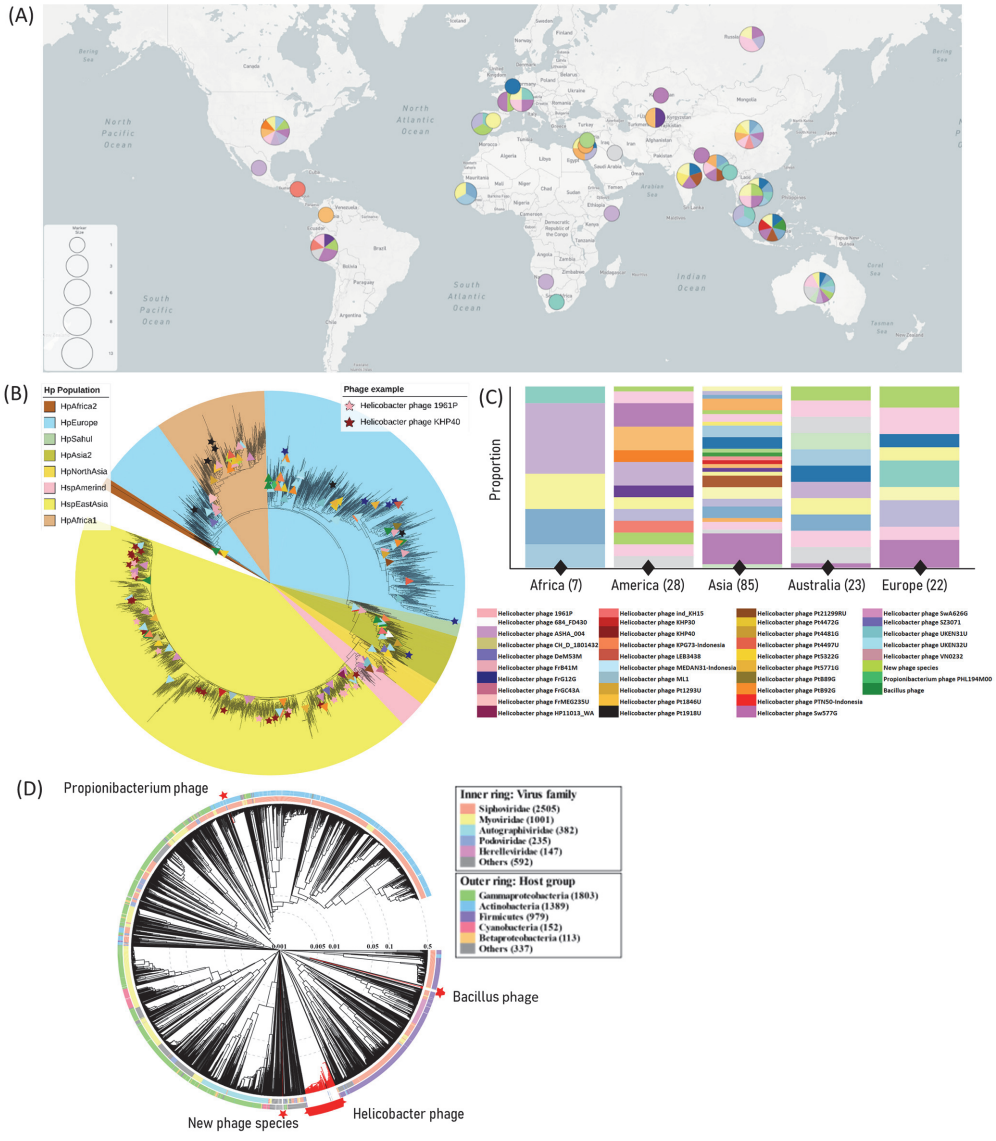
**Background** Although the study of bacteriophages has recently increased, the knowledge about phages in *Helicobacter pylori* remains limited. We conducted a global-scale study to understand their worldwide distribution, genetic feature, and impacts on antimicrobial resistance (AMR) along with clinical disease profiles. We also tried to find a new valuable candidate for phage-based therapy.

**Methods** We performed in-depth genome analysis through 1979 clinical *H.pylori*, retrieved from 68 countries worldwide. Phage identification and further investigation were identified using well-established tools. We analyzed their clinical impact using 552 antibiogram data of six antibiotics and 258 clinical-histological data. Both data were retrieved from *H.pylori*-infected patients across multi nations.

**Results** We successfully identified 1075 phage elements and 165 intact phages. The intact phages mostly tended to become virulent (58.18;96/165) than remain temperate (41.81;69/165). Most temperate phages were active (62.32;43/69). We found 16 novel bacteriophages, including two novel-phage species. We demonstrated for the first time that their distribution was correlated with geographical and




**Abstract IDDF2022-ABS-0155 Figure 1**

ancestral populations, with some initially reported from non-Helicobacter phage (IDDF2022-ABS-0155 Figure 1. Phage distribution and novel bacteriophage species and strains A phage distribution based on the geographical area B phage distribution based on the H pylori ancestral popul). Helicobacter phage had different GC content than non-Helicobacter phage. The GC content variation of Helicobacter phage was correlated with the GC content of the *H.pylori* chromosome ($r$=0.525; $p$<0.001). Thus, the GC content variation may associate with the phage host specification and their integration site. We showed that around 10% of helicobacter-phage harboured genes related to AMR. We proved that helicobacter-phage correlated with *H.pylori* AMR phenotype. The MIC value of Ciprofloxacin and Clarithromycin was significantly higher in strains with phage than those without phage ($p$=0.014 and 0.034, respectively). Next, patients infected with strains containing phage tended to have lower histological findings, especially on the proinflammatory cell infiltration ($p$<0.001) and intestinal metaplasia score ($p$<0.003). In addition, our results suggested that Helicobacter phage UKEN32U may be suitable as a candidate for phage-based therapy.

**Conclusions** Our study highlights the importance of phage identification in clinical *H.pylori* isolate. They were widely distributed, could harbour AMR genes, and were related to AMR development and clinical outcome.

## IDDF2022-ABS-0219 RECOVERY OF THE GUT MICROBIOTA UNDER ORAL IRON SUPPLEMENTATION IS DELETERIOUS AND PROMOTES COLORECTAL CARCINOGENESIS IN *APC$^{MIN/+}$* MICE

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**Background** Colorectal cancer (CRC) induces anemia in a large proportion of patients and is usually treated with oral iron supplementation. Surgery, the main treatment for CRC, is routinely accompanied by prophylactic antibiotics to avoid infection. However, the combined effect of antibiotics and luminal iron in the gut on the microbiota and intestinal homeostasis remains unknown.

**Methods** Wild-type (WT) mice were subjected to antibiotic treatment followed by oral iron supplementation at different concentrations. The composition of the gut microbiota and its recovery were assessed by 16S rRNA sequencing of the stool. Short-chain fatty acid (SCFA) concentrations were also assessed in the stool. In addition, *APC$^{Min/+}$* mice (a CRC mouse model) received fecal microbiota transplantation (FMT) using samples from anemic CRC patients, followed by oral iron supplementation at different concentrations. Tumor burden and Ki-67-positive colonic cells were quantified, and gut microbiota composition was assessed by 16S rRNA sequencing.

**Results** In WT mice, recovery from antibiotics under high luminal iron concentration shifted the gut microbiota toward a Bacteroidetes phylum-dominant composition. Three bacterial species characterized as CRC markers and/or CRC initiators were more abundant under oral iron supplementation and showed a lack of recovery of fecal concentrations of butyrate, an SCFA that inhibits cancer cell proliferation. *APC$^{Min/+}$* mice that received FMT from anemic CRC patients under oral iron supplementation developed more colonic tumors and had a higher proportion of Ki-67-positive cells compared to *APC$^{Min/+}$* fed an iron sufficient diet.

**Conclusions** Gut microbiota recovery from antibiotic exposure under oral iron supplementation is frequent in CRC patients but is also common in the general population. This study identifies possible deleterious effects of the concomitance of these two disruptive agents of the gut microbiota and may lead to modifications in the management of anemia in patients with CRC.

## IDDF2022-ABS-0230 IMPACT OF URBANIZATION ON PREVALENCE OF ADHERENT-INVASIVE ESCHERICHIA COLI IN CROHN'S DISEASE PATIENTS: CAUSE FOR PATHOGENESIS?

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**Background** The incidence of Crohn's disease (CD) has increased drastically in newly industrialised countries with rapid urbanization. The colonisation of adherent-invasive *Escherichia coli* (AIEC) was associated with CD pathogenesis and the presence of AIEC closely correlated with mucosal *E. coli* load. In this study, we aimed to identify risk factors for AIEC colonization in CD patients and determine the effect of urbanization on AIEC prevalence.

**Methods** A total of 137 CD patients were recruited from Yunnan (rural China) and Hong Kong (urban China). Clinical questionnaires and ileal biopsy samples were collected during colonoscopies. Patient were categorised as high *E.coli* load (colony-forming units (CFU) > 300), low *E.coli* load (CFU ≤ 300) and *E.coli* negative (CFU = 0). Statistical significance for continuous and categorical variables was calculated by the Kruskal-Wallis test and Pearson's chi-squared test in univariate analysis. The association between individual-level factors and log-transformed *E.coli* CFU was assessed using multivariate regression. Mucosal *E.coli* prevalence was compared in rural and urban regions and Ordinal Logistic Regression was used to evaluate the risk of urbanization on mucosal *E.coli* prevalence.

**Results** Among individual-level factors, a surgery history (P = 0.019) was significantly associated with different *E.coli* prevalence (IDDF2022-ABS-0230 Table 1). Multivariate analysis showed that a past surgical history (Beta = -3.12, P = 0.01) was negatively correlated with mucosal *E.coli* while age was positively associated with mucosal *E.coli* (Beta = 0.09, P = 0.04) in CD patients. The prevalence of mucosal